=>

#### (FILE 'HOME' ENTERED AT 12:06:14 ON 03 JUL 2006)

```
FILE 'MEDLINE, AGRICOLA, BIOSIS, CAPLUS, EMBASE, SCISEARCH' ENTERED AT
     12:06:24 ON 03 JUL 2006
                E HOLM J/AU
L1
           1609 E3
                E HOLM JENS/AU
             14 E3
L2
                E IPSEN H/AU
L3
            295 E3 OR E5 OR E8
                E LARSEN J/AU
L4
           1162 E3
                E LARSEN J N/AU
            169 E3
L5
                E LARSEN JORGEN/AU
             33 E8 OR E12
L6
                E LARSEN JORGEN NEDERGAARD
                E LARSEN JORGEN NEDERGAARD/AU
L7
             11 E3
                E LARSEN JORGEN/AU
L8
              8 E3
                E SPANGFORT M/AU
L9
            289 E3 OR E4 OR E5 OR E6 OR E7
L10
           3337 L1 OR L2 OR L3 OR L4 OR L5 OR L6 OR L7 OR L8 OR L9
L11
        137845 ALLERGEN OR ALLERGENS
L12
        6852731 (MUTANT OR MUTATED OR HYBRID OR VARIANT OR MODFY OR MODIFIED OR
L13
           2780 L11(S)L12
L14
             48 L13 AND L10
L15
             20 DUP REM L14 (28 DUPLICATES REMOVED)
        165175 IGE OR (IMMUNOGLOBULIN(W)E)
L16
        6588415 BIND OR BINDING OR BOUND OR CAPACITY OR RECOGNITION OR EPITOPE
L17
L18
              0 L16(S)_L17
L19
          22837 L16(S) L17
L20
           5283 L19 (S) (REDUCE OR REDUCTION OR DIMINISH OR DIMUNITION OR DECRE
L21
            375 L20(S) L12
L22
            262 L21(P)L11
L23
           140 L21(S)L11
L24
            55 DUP REM L23 (85 DUPLICATES REMOVED)
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## **EAST Search History**

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	12815	allergen or allergens	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:26
L2	1054	allergenicity	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:26
L3	3946955	mutant or mutated or modified or modification or variant or derivative or dervitization or altered	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:32
L4	22146	IgE or (immunoglobulin adj E)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:28
L5	5016253	bind or binding or bound or recognition or capacity or recognize or capable or capability or reactive or reactivity	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:31
L6	3955729	mutant or mutated or modified or modification or variant or derivative or dervitization or altered or mutation	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:32
L7	189442	angstrom or angstroms or nanometere or nanometers	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:33
L8	6940209	inhibit or inhibition or reduce or reduction or diminish or dimunition or decrease or decreased or inhibited or reduced or diminished	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:34
L9	1077	I6 with I1	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:35
L10	538	18 with 12	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:35
L11	4316	I4 with I5	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:35

## **EAST Search History**

L12	792	18 with 111	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:35
L13	82	19 same 110	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:36
L14	211	19 same 111	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:36
L15	81	l9 same l12	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:36
L16	13	17 and (113 or 114 or 115)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/07/03 12:37

## **SCORE Search Results Details for Application** 10001245 and Search Result us-10-001-245c-36.rai.

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This page gives you Search Results detail for the Application 10001245 and Search Result us-10-001-245c-36.rai.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 26, 2006, 10:07:39; Search time 26 Seconds (without alignments)

434.287 Million cell updates/sec

Title:

US-10-001-245C-36

Perfect score: 692

Sequence:

1 DQVDVKDCANHEIKEVLVPG......VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:\* 2: /EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:\* 3: /EMC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\* 5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS COMB.pep:\* /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

/EMC Celerra SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

Score Match Length DB ID

용

Description

1	638	92.2	145	2	US-09-949-889-3	Sequence	3, Appli
2	635	91.8	145	2	US-08-460-040-6		6, Appli
3	635	91.8	146	1	US-07-945-288-4		4, Appli
4	635	91.8	146	1	US-08-462-831-4		4, Appli
5	635	91.8	146	1	US-08-461-809-4		4, Appli
6	635	91.8	146	1	US-08-461-441-4	Sequence	4, Appli
7	635	91.8	146	1	US-08-482-142-4	Sequence	4, Appli
8	635	91.8	146	1	US-08-478-572-4	Sequence	4, Appli
9	635	91.8	146	2	US-08-484-296-4	Sequence	4, Appli
10	635	91.8	146	5	PCT-US93-08518-4		4, Appli
11	627	90.6	129	1	US-08-462-831-12	Sequence	12, Appl
12	627	90.6	129	1	US-08-461-809-12	Sequence	12, Appl
13	627	90.6	129	1	US-08-461-441-12	Sequence	12, Appl
14	627	90.6	129	5	PCT-US93-08518-12		12, Appl
15	622	89.9	129	1	US-07-945-288-12	Sequence	12, Appl
16	621	89.7	129	2	US-09-949-889-4	Sequence	4, Appli
17	603	87.1	129	1	US-08-482-142-157		157, App
18	603	87.1	129	1	US-08-478-572-157		157, App
19	603	87.1	129	2	US-08-484-296-157	Sequence	157, App
20	596	86.1	129	1	US-08-482-142-159		159, App
21	596	86.1	129	1	US-08-478-572-159	Sequence	159, App
22	596	86.1	129	2	US-08-484-296-159	-	159, App
23	592	85.5	129	2	US-08-930-264-4		4, Appli
24	590.5	85.3	130	1	US-08-482-142-158	Sequence	158, App
25	590.5	85.3	130	1	US-08-478-572-158	Sequence	158, App
26	590.5	85.3	130	2	US-08-484-296-158		158, App
27	590	85.3	129	2	US-08-930-264-6		6, Appli
28	590	85.3	129	2	US-08-930-264-16		16, Appl
29	590	85.3	129	2	US-08-930-264-20		20, Appl
30	590	85.3	142	1	US-08-288-888-4		4, Appli
31	590	85.3	142	1	US-08-910-075-4		4, Appli
32	590	85.3	142	1	US-08-905-801A-4	<del>-</del>	4, Appli
33	589	85.1	129	2	US-08-930-264-18	•	18, Appl
34	588	85.0	129	2	US-08-930-264-2		2, Appli
35	588	85.0	142	1	US-08-288-888-2		2, Appli
36	588	85.0	142	1	US-08-910-075-2	-	2, Appli
37	588	85.0	142	1	US-08-905-801A-2		2, Appli
38	587	84.8	129	2	US-08-930-264-24		24, Appl
39	586	84.7	129	2	US-08-930-264-8		8, Appli
40	585	84.5	129	1	US-07-945-288-8		8, Appli
41	585	84.5	129	1	US-08-462-831-8	•	8, Appli
42	585	84.5	129	1	US-08-461-809-8		8, Appli
43	585	84.5	129	1	US-08-461-441-8		8, Appli
44	585	84.5	129	1	US-08-482-142-8		8, Appli
45	585	84.5	129	1	US-08-478-572-8	Sequence	8, Appli

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RESULT 1
US-09-949-889-3
; Sequence 3, Application US/09949889
; Patent No. 6800290
; GENERAL INFORMATION:
; APPLICANT: CONSIGLIO NAZIONALE DELLE RICERCHE
  TITLE OF INVENTION: VARIANTS OF ALLERGENIC PROTEINS OF THE GROUP 2 OF
  TITLE OF INVENTION: DERMATOPHAGOIDES
  FILE REFERENCE: Cons Naz Ric
; CURRENT APPLICATION NUMBER: US/09/949,889
```

# **SCORE Search Results Details for Application** 10001245 and Search Result us-10-001-245c-36.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: June 26, 2006, 10:18:54; Search time 184 Seconds

(without alignments)

324.754 Million cell updates/sec

US-10-001-245C-36 Title:

Perfect score: 692

Sequence: 1 DQVDVKDCANHEIKEVLVPG......VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 segs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:\* 2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:\* 3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\* 5: /EMC Celerra SIDS3/ptodata/2/pubpaa/US10B PUBCOMB.pep:\* 6: /EMC Celerra SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ક Result Query

No. Score Match Length DB ID Description

1	692	100.0	129	4	US-10-001-245-36	Seguence	36, Appl
2	684	98.8	129	4	US-10-001-245-40		40, Appl
3	684	98.8	129	4	US-10-001-245-46	-	46, Appl
4	683	98.7	129	4	US-10-001-245-42	-	42, Appl
5	683	98.7	129	4	US-10-001-245-44	<u> </u>	44, Appl
6	682	98.6	129	4	US-10-001-245-38	-	38, Appl
7	665	96.1	129	4	US-10-001-245-48		48, Appl
8	657	94.9	129	4	US-10-001-245-52	_	52, Appl
9	657	94.9	129	4	US-10-001-245-54		54, Appl
10	657	94.9	129	4	US-10-001-245-58	<del>-</del>	58, Appl
11	656	94.8	129	4	US-10-001-245-56	<del>-</del>	56, Appl
12	655	94.7	129	4	US-10-001-245-50	-	50, Appl
13	648	93.6	129	4	US-10-001-245-94		94, Appl
14	646	93.4	129	4	US-10-001-245-171		171, App
15	643	92.9	129	4	US-10-001-245-169		169, App
16	641	92.6	129	4	US-10-001-245-168		168, App
17	638	92.2	129	4	US-10-001-245-170	<del>-</del>	170, App
18	638	92.2	145	3	US-09-949-889-3	_	3, Appli
19	635	91.8	129	4	US-10-001-245-90		90, Appl
20	635	91.8	129	4	US-10-698-855-8		8, Appli
21	635	91.8	136	5	US-10-799-514-17		17, Appl
22	635	91.8	146	3	US-09-877-160-3		3, Appli
23	635	91.8	146	3	US-09-847-208-80		80, Appl
24	635	91.8	146	4	US-10-001-245-138		138, App
25	635	91.8	146	5	US-10-809-689-20		20, Appl
26	635	91.8	146	5	US-10-498-026-14		14, Appl
27	631	91.2	129	4	US-10-001-245-167		167, App
28	629	90.9	128	4	US-10-001-245-172		172, App
29	629	90.9	129	3	US-09-957-806A-8	<del>-</del>	8, Appli
30	621	89.7	129	3	US-09-949-889-4	-	4, Appli
31	596	86.1	146	4	US-10-001-245-173		173, App
32	594	85.8	138	4	US-10-001-245-174		174, App
33	592	85.5	129	4	US-10-001-245-175		175, App
34	592	85.5	146	3	US-09-847-208-74		74, Appl
35	592	85.5	146	5	US-10-809-689-28		28, Appl
36	592	85.5	146	5	US-10-498-026-22		22, Appl
37	590	85.3	129	4	US-10-001-245-176		176, App
38	588	85.0	129	3	US-09-957-806A-7		7, Appli
39	576	83.2	135	4	US-10-001-245-178	<del>-</del>	178, App
40	575	83.1	145	4	US-10-001-245-177		177, App
41	365	52.7	73	5	US-10-799-514-16		16, Appl
42	365	52.7	159	5	US-10-799-514-23		23, Appl
43	352.5	50.9	153	5	US-10-799-514-22	-	22, Appl
44	348	50.3	72	5	US-10-799-514-15		15, Appl
45	272.5	39.4	126	3	US-09-860-793-1		1, Appli
		<del>-</del>		-	<del>-</del>		

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RESULT 1
US-10-001-245-36
; Sequence 36, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
```

# SCORE Search Results Details for Application 10001245 and Search Result us-10-001-245c-36.rapbn.

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

June 26, 2006, 10:19:19; Search time 23 Seconds (without alignments)

128.134 Million cell updates/sec

Title:

US-10-001-245C-36

Perfect score: 692

Sequence: 1 I

1 DQVDVKDCANHEIKEVLVPG.....VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 99297

99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

8: /EMC Celerra SIDS3/ptodata/2/pubpaa/US60 NEW PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	635	91.8	129	7	US-11-256-589-1	Sequence 1, Appli
2	592	85.5	129	7	US-11-256-589-2	Sequence 2, Appli
3	575	83.1	129	7	US-11-256-589-3	Sequence 3, Appli
4	71	10.3	269	6	US-10-953-349-20341	Sequence 20341, A
5	71	10.3	362	6	US-10-953-349-20340	Sequence 20340, A
6	71	10.3	400	6	US-10-953-349-20339	Sequence 20339, A
7	70.5	10.2	534	6	US-10-449-902-55332	Sequence 55332, A
8	67.5	9.8	1723	6	US-10-486-020-6	Sequence 6, Appli
9	67	9.7	474	6	US-10-953-349-13788	Sequence 13788, A
10	67	9.7	482	6	US-10-953-349-13787	Sequence 13787, A
11	67	9.7	495	6	US-10-953-349-13786	Sequence 13786, A
12	66	9.5	153	6	US-10-953-349-6205	Sequence 6205, Ap
13	66	9.5	909	6	US-10-449-902-44686	Sequence 44686, A
14	64.5	9.3	314	6	US-10-953-349-28060	Sequence 28060, A
15	64.5	9.3	347	6	US-10-953-349-28059	Sequence 28059, A
16	64.5	9.3	404	6	US-10-449-902-30010	Sequence 30010, A
17	64.5	9.3	404	6	US-10-449-902-37192	Sequence 37192, A
18	64.5	9.3	404	6	US-10-449-902-49380	Sequence 49380, A
19	64.5	9.3	517	6	US-10-449-902-54954	Sequence 54954, A
20	64.5	9.3	912	7	US-11-121-154-203	Sequence 203, App
21	64	9.2	191	6	US-10-449-902-29716	Sequence 29716, A
22	64	9.2	381	6	US-10-449-902-56442	Sequence 56442, A
23	63.5	9.2	496	6	US-10-449-902-36894	Sequence 36894, A
24	63.5	9.2	496	6	US-10-449-902-37114	Sequence 37114, A
25	63.5	9.2	702	6	US-10-538-066-363	Sequence 363, App
26	63.5	9.2	1674	6	US-10-542-516-18	Sequence 18, Appl
27	63	9.1	180	6	US-10-953-349-23280	Sequence 23280, A
28	63	9.1	215	6	US-10-953-349-23279	Sequence 23279, A
29	63	9.1	531	6	US-10-449-902-38747	Sequence 38747, A
30	62.5	9.0	333	6	US-10-449-902-47096	Sequence 47096, A
31	62.5	9.0	601	6	US-10-449-902-34688	Sequence 34688, A
32	62.5	9.0	641	7	US-11-340-715-11	Sequence 11, Appl
33	62	9.0	1028	6	US-10-449-902-55810	Sequence 55810, A
34	62	9.0	1118	6	US-10-449-902-43544	Sequence 43544, A
35	61.5	8.9	404	6	US-10-449-902-46039	Sequence 46039, A
36	61.5	8.9	416	7	US-11-264-784-363	Sequence 363, App
37	61.5	8.9	416	7	US-11-264-737-50	Sequence 50, Appl
38	61.5	8.9	416	7	US-11-265-761-380	Sequence 380, App
39	61.5	8.9	738	6	US-10-449-902-51852	Sequence 51852, A
40	61.5	8.9	822	6	US-10-953-349-4066	Sequence 4066, Ap
41	61.5	8.9	870	6	US-10-953-349-4065	Sequence 4065, Ap
42	61.5	8.9	1008	6	US-10-449-902-50438	Sequence 50438, A
43	61.5	8.9	1050	6	US-10-953-349-4064	Sequence 4064, Ap
44	61	8.8	383	6	US-10-953-349-21898	Sequence 21898, A
45	61	8.8	406	6	US-10-449-902-50101	Sequence 50101, A

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RESULT 1
US-11-256-589-1
; Sequence 1, Application US/11256589
; Publication No. US20060121063A1
; GENERAL INFORMATION:
; APPLICANT: Roggen, Erwin Ludo
; APPLICANT: Friis, Esben Peter
; APPLICANT: Soni, Nanna Kristensen
; APPLICANT: Draborg, Henriette
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# SCORE Search Results Details for Application 10001245 and Search Result us-10-001-245c-36.rapm.

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```
GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 26, 2006, 10:08:04; Search time 607 Seconds

(without alignments)

324.510 Million cell updates/sec

Title: US-10-001-245C-36

Perfect score: 692

Sequence: 1 DQVDVKDCANHEIKEVLVPG......VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8366291 segs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending Patents AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/paa/PCTUS\_COMB.pep:\*
2: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US066\_COMB.pep:\*
3: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US073\_COMB.pep:\*
4: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US074\_COMB.pep:\*
5: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US075\_COMB.pep:\*
6: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US076\_COMB.pep:\*
7: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US077\_COMB.pep:\*
8: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US078\_COMB.pep:\*
9: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US079\_COMB.pep:\*
10: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US079\_COMB.pep:\*
11: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US080\_COMB.pep:\*
12: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US081\_COMB.pep:\*
13: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US082\_COMB.pep:\*
14: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US083\_COMB.pep:\*
15: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US084\_COMB.pep:\*
15: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US085\_COMB.pep:\*

/EMC\_Celerra\_SIDS3/ptodata/2/paa/US086 COMB.pep:\*

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17:
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     /EMC Celerra SIDS3/ptodata/2/paa/US088 COMB.pep:*
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     /EMC Celerra SIDS3/ptodata/2/paa/US090 COMB.pep:*
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     /EMC Celerra SIDS3/ptodata/2/paa/US606 COMB.pep:*
51:
     /EMC Celerra SIDS3/ptodata/2/paa/US607 COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

			8					
R	esult		Query					
	No.	Score	Match	Length	DB	ID	Description	
	1	692	100.0	129	30	US-10-001-245-36	Sequence 36,	Appl
	2	692	100.0	129	30	US-10-001-245B-36	Sequence 36,	Appl
	3	692	100.0	129	30	US-10-001-245C-36	Sequence 36,	Appl
	4	684	98.8	129	30	US-10-001-245-40	Sequence 40,	Appl
	5	684	98.8	129	30	US-10-001-245-46	Sequence 46,	Appl
	6	684	98.8	129	30	US-10-001-245B-40	Sequence 40,	Appl
	7	684	98.8	129	30	US-10-001-245B-46	Sequence 46,	Appl
	8	684	98.8	129	30	US-10-001-245C-40	Sequence 40,	Appl
	9	684	98.8	129	30	US-10-001-245C-46	Sequence 46,	Appl
	10	683	98.7	129	30	US-10-001-245-42	Sequence 42,	Appl
	11	683	98.7	129	30	US-10-001-245-44	Sequence 44,	Appl
	12	683	98.7	129	30	US-10-001-245B-42	Sequence 42,	Appl
	13	683	98.7	129	30	US-10-001-245B-44	Sequence 44,	Appl
	14	683	98.7	129	30	US-10-001-245C-42	Sequence 42,	Appl
	15	683	98.7	129	30	US-10-001-245C-44	Sequence 44,	Appl

# SCORE Search Results Details for Application 10001245 and Search Result us-10-001-245c-36.rapn.

Score HomeRetrieve ApplicationSCORE SystemPageListOverview

RE System SCORE rview FAQ

Comments / Suggestions

This page gives you Search Results detail for the Application 10001245 and Search Result us-10-00 245c-36.rapn.

<u>start</u>

Go Back to previou

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 26, 2006, 10:08:39; Search time 25 Seconds

(without alignments)

195.510 Million cell updates/sec

Title: US-10-001-245C-36

Perfect score: 692

Sequence: 1 DQVDVKDCANHEIKEVLVPG......VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 165654 segs, 37889597 residues

Total number of hits satisfying chosen parameters: 165654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Pending Patents AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*
2: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US06\_NEW\_COMB.pep:\*
3: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US07\_NEW\_COMB.pep:\*
4: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US08\_NEW\_COMB.pep:\*
5: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US09\_NEW\_COMB.pep:\*
6: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US10\_NEW\_COMB.pep:\*
7: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US11\_NEW\_COMB.pep:\*
8: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	112	16.2	151	7	US-11-431-708-1795	Sequence 1795, Ap
2	112	16.2	151	7	US-11-431-708-1796	Sequence 1796, Ap
3	112	16.2	151	7	US-11-431-708-1798	Sequence 1798, Ap
4	112	16.2	199	7	US-11-431-708-1797	Sequence 1797, Ap
5	76.5	11.1	504	7	US-11-431-855-29372	Sequence 29372, A
6	72	10.4	371	6	US-10-579-025-4	Sequence 4, Appli
7	72	10.4	1049	7	US-11-431-855-26182	Sequence 26182, A
8	71.5	10.3	388	5	US-09-674-546B-2568	Sequence 2568, Ap
9	68.5	9.9	957	7	US-11-431-708-3553	Sequence 3553, Ap
10	68.5	9.9	957	7	US-11-431-708-3554	Sequence 3554, Ap
11	68	9.8	374	7	US-11-431-855-16075	Sequence 16075, A
12	68	9.8	2405	7	US-11-431-855-22750	Sequence 22750, A
13	67.5	9.8	952	1	PCT-US03-41389-709	Sequence 709, App
14	67.5	9.8	956	6	US-10-579-802-70	Sequence 70, Appl
15	67.5	9.8	1233	7	US-11-431-708-876	Sequence 876, App
16 17	67.5	9.8	1723	7 7	US-11-431-708-1218	Sequence 1218, Ap
17 18	67.5 67.5	9.8 9.8	1723 2346	7	US-11-431-708-1219	Sequence 1219, Ap
19	67.3	9.7	2494	6	US-11-431-708-1217 US-10-669-920-22	Sequence 1217, Ap
20	66.5	9.6	896	6	US-10-774-721B-10	Sequence 22, Appl Sequence 10, Appl
21	66.5	9.6	896	7	US-11-439-325-3	Sequence 3, Appli
22	66.5	9.6	923	7	US-11-439-325-4	Sequence 4, Appli
23	66.5	9.6	1161	6	US-10-774-721B-14	Sequence 14, Appl
24	66.5	9.6	1165	7	US-11-439-325-2	Sequence 2, Appli
25	66.5	9.6	1165	7	US-11-377-486-56	Sequence 56, Appl
26	66.5	9.6	1234	6	US-10-774-721B-12	Sequence 12, Appl
27	66.5	9.6	3487	7	US-11-431-855-33557	Sequence 33557, A
28	66	9.5	388	7	US-11-431-708-1657	Sequence 1657, Ap
29	66	9.5	403	7	US-11-431-708-1656	Sequence 1656, Ap
30	65.5	9.5	386	7	US-11-431-855-9730	Sequence 9730, Ap
31	65.5	9.5	388	5	US-09-674-546B-1868	Sequence 1868, Ap
32	65.5	9.5	388	5	US-09-674-546B-1870	Sequence 1870, Ap
33	65.5	9.5	388	5	US-09-674-546B-2570	Sequence 2570, Ap
34	65.5	9.5	388	5	US-09-674-546B-2572	Sequence 2572, Ap
35	65.5	9.5	389	7	US-11-431-855-33115	Sequence 33115, A
36	65	9.4	2556	6	US-10-720-896B-11	Sequence 11, Appl
37	65	9.4	2578	7	US-11-431-855-22839	Sequence 22839, A
38	63.5	9.2	219	7	US-11-431-855-26697	Sequence 26697, A
39	63.5	9.2	372	6	US-10-579-007-4	Sequence 4, Appli
40 41	63.5	9.2	702	1	PCT-US06-00944A-282	Sequence 282, App
41 42	63.5 63.5	9.2 9.2	702 702	6 7	US-10-545-515A-7	Sequence 7, Appli
42	63.5	9.2	702	7	US-11-318-418-136 US-11-318-418-136	Sequence 136, App
44	63.5	9.2	702	7	US-11-316-416-136 US-11-431-708-3544	Sequence 136, App Sequence 3544, Ap
45	63.5	9.2	702	7	US-11-431-708-3544 US-11-431-708-3545	Sequence 3545, Ap
7.0	03.3	٥. ٧	102	,	OD II 401 - 100-2040	peditetice anan' Wh

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RESULT 1
US-11-431-708-1795
; Sequence 1795, Application US/11431708
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven
  TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
  FILE REFERENCE: CL001599-ORD
; CURRENT APPLICATION NUMBER: US/11/431,708
; CURRENT FILING DATE: 2006-05-11
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